REMARKS

Applicant respectfully requests reconsideration of the present application in view of the foregoing amendments and in view of the reasons that follow.

Drawing Amendments

Applicants submit herewith a corrected Figure 8 entitled "Replacement Sheet." Applicants understand that the original of the photocopy is too dark and therefore a new, lighter copy is submitted. No new matter has been presented by this amended drawing and Applicants request its entry.

Specification Amendments

Paragraph [00126] has been amended to address the objections discussed below. Specifically, a number of terms have been objected to as allegedly being unclear or vague. These terms have been clarified with this amendment.

Applicants submit that no new matter has been added by this amendment and respectfully request its entry.

Claim Amendments

The claims have been amended to reflect that the invention is directed to quantitatively analyzing 3 to 8 samples of molecules simultaneously. Support for this amendment may be found in the specification, for example, on page 6 [0022], where it is described that at least 3 samples can be analyzed. Further support for this amendment, may be found, in the specification, for example on page 19 [0097] wherein 8 combinations of differentially labelled reagents are listed. Claims 4, 6, 8-10, 12-14, 21, 33-34, and 36 have been amended accordingly.

Claims 33, 34 and 36 have been further amended to clarify that there is one combination of labelled reagents for each sample. Each combination of reagents is unique in that the members are isotopically distinct. This concept is best explained by a review of Table 1 on page

19 of the specification as filed. The table describes 8 different combinations of reagents that are isotopically distinct. The methods of the invention, require that there is one combination of reagents provided for each the samples. The samples are then reacted with the reagents to provide 3 to 8 samples of isotope-labelled derivatives.

Claims 28 and 32 have been canceled. As such, any claims previously depending from claim 32 have been amended to depend from other pending claims. Applicants specifically reserve the right to file a continuation and/or divisional application directed to the canceled subject matter.

Applicants submit that no new matter has been added by this amendment and as such, request its entry.

After amending the claims as set forth above, claims 4-14, 17-23 and 33-36 are now pending in this application.

Objections to the Specification

The Office has objected to a number of items in paragraphs [00126] and [00127].

1. The Office has objected to the phrase "each sample" in sentence 2 as allegedly being vague. This term has been replaced by "each labelled amine." Support for this amendment is from the description of columns 3 and 4 of Table 2. Specifically, these columns describe masses of labelled compounds.

2. The Office has objected to the phrase "the molecules" in sentence 3 as allegedly being vague. This term has been replaced by "labelled amines." It is clear that this term was intended based on the previous sentence and the description of columns 3 and 4.

3. The Office has objected to the phrase "API III+" in sentence 4 as allegedly being vague. This term refers to a model name of a triple quadrupole mass spectrometer manufactured

by PE-Sciex (now MDS Analytical Technologies). Applicants submit that this term is known and understood by those of skill in the art.

4. The Office has objected to the phrase "IonSpray" in sentence 4 as allegedly being vague. The phrase has been amended to include that it is an unregistered trademark and also the term source has been capitalized. Information about this product can be found at https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=600892. (A copy of the webpage is enclosed herewith). Ionspray is listed in claim 7 as one type of electrospray ionization.

5. The Office has objected to the phrase "the amines" in sentence 6 as allegedly lacking basis in prior sentences. Applicants have added the phrase "that were labelled."

6. The Office has objected to the phrase "various amines" in paragraph [00127] as allegedly being vague. In light of the other clarifying amendments to paragraph [00126], this term is now clear. Further, the title of the table "Analysis of various amines" is consistent with the terminology used in the field of analytical chemistry where one refers to the analytes in their native state not to the labelled form, as the latter are created for the purposes of facilitating the analysis.

7. The Office has objected to Table 2 as allegedly failing to indicate whether cyanoborohydride or cyanoborodeuteride is used and also because Applicants did not indicate how the "stuff" was weighed in columns 3 and 4. First, although Table 2 does not specifically indicate which reducing agent is used, the paragraph describing the contents of the table, specifically sentence 12 of paragraph [00126] states that "$NaCNBH_3$", i.e. sodium cyanoborohydride, was used.

Applicants submit that although it is not specifically discussed how the samples were weighed, this is a task that is well within the skill of the art. In addition, the specific

concentrations, solvents and pH of solutions prepared are described in detail in paragraph [00112] of the specification as filed.

Applicants submit that in light of the amendments to paragraph [00126] and the above remarks, this paragraph in the specification is now clear. Thus, Applicants respectfully request that the rejection be withdrawn.

Drawings

The drawings have been objected to because the lower panel of Fig. 8 allegedly fails to show "3-aminothiophenol labelled with CH_2O (m/z = 123.0) and CD_2O (m/z = 127.0) and $NaCNBH_3$" as described in the specification, sentence 12.

Applicants thank the Examiner for pointing this out. The Examiner is correct that the expected mass to charge ratio shown is not that for 3-aminothiophenol. In fact, this was a typographical error. The data shown in Figure 8 corresponds to 3-aminopyridine. Applicants would appreciate if the Examiner would comment on whether or not an inventor declaration would help to clarify the record.

Additionally, Figure 8 has been objected to as the chemical structures are too dark. Applicants submit herewith a corrected drawing.

Claim Rejections under 35 U.S.C. § 112, first paragraph

Claims 4-14, 17-23 and 32-36 have been rejected as allegedly failing to comply with the written description requirement. The Action on page 5 states:

> Specifically, independent claims 32, 33 and 36, as amended, are directed to methods comprising, inter alia, labelling reagents containing [an] aldehyde AND reducing agent. Examiner is unable to locate support in Applicant's original specification for labeling reagents containing aldehyde AND reducing agent. Examiner is unable to locate support in Applicant's original specification for methods incorporated labelling reagents containing aldehyde AND reducing agent...Applicants'

> description of 'sample in the presence of the reducing agent' is not equivalent to the claimed aldehyde AND reducing agent required in step (i) of claims 32, 33, and 36.

To satisfy the written description requirement, a patent specification must describe the claimed invention in sufficient detail that one skilled in the art can reasonably conclude that the inventor had possession of the claimed invention. See, e.g., *Moba, B.V. v. Diamond Automation, Inc.*, 325 F.3d 1306, 1319, 66 USPQ2d 1429, 1438 (Fed. Cir. 2003); *Vas-Cath, Inc. v. Mahurkar*, 935 F.2d at 1563, 19 USPQ2d at 1116.

Applicants submit that the use of an aldehyde AND a reducing agent is adequately described in the specification and therefore, requiring an aldehyde and a reducing agent in the claimed methods is not new matter. Specifically, on page 7, [0031] of the specification, it is taught that "[t]he isotopically labelled reagents may be an aldehyde and a reducing agent." Further on page 12, [0071], it is taught that "[t]he method involves the reductive alkylation of amine groups to their alkylamine derivatives by the action of an added aldehyde (for example formaldehyde) and a reducing agent, optionally a Schiff based reducing agent, for example sodium cyanoborohydride." Still further examples of using an aldehyde and a reducing agent are described in the specification, see, for example, page 14 [0079], page 16 [0088], page 17 [0089], and Table 1 on page 19 [0097], page 26 [00120], page 28 [00125], etc. Examples 7, 8, and 9 of the specification provide examples of combinations comprising both a reducing agent and an aldehyde.

In light of the above, there is adequate support to claim the use of an aldehyde and a reducing agent. As such, Applicants respectfully request withdrawal of this rejection.

Claim Rejection under 35 U.S.C. § 112, first paragraph

Claims 4-14, 17-23 and 32-36 stand rejected for allegedly failing to comply with the enablement requirement. According to the Office, the claims contain subject matter not described in the specification in a way to enable one skilled in the art to which it pertains, or with which it is mostly connected, to make or use the invention.

The test of enablement is whether the applicants have taught how to make and use the invention as claimed.

> As a matter of Patent Office practice... a specification disclosure which contains a teaching of the manner and process of making and using the invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented *must* be taken as in compliance with the enabling requirement of the first paragraph of §112 *unless* there is reason to doubt the objective truth of the statements contained therein which must be relied on for enabling support. In re Marzocchi, 439 F.2d 220, 223-24, 169 USPQ 367, 369-70 (CCPA 1971).

Further the court in *Marzocchi* has stated, "it is incumbent upon the Patent Office, whenever a rejection on this basis is made, to explain why it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement." MPEP 2164.04; In re Marzocchi, 439 F.2d 220, 169 USPQ 367 (CCPA 1971).

Applicants submit that the Office has not met its initial burden of showing that the claims are not enabled. Applicants also submit that the specification teaches that the claimed methods can be performed by one of skill in the art without undue experimentation.

As stated above, the methods of the invention are directed to methods of quantitatively analyzing 3 to 8 samples of molecules which have an amine group bearing an active hydrogen. This is done by reacting the amine groups with a aldehyde and a reducing agent. This reaction is either called reductive amination or reductive alkylation of the amine. Each of the samples is reacted with a different combination of an aldehyde and a reducing agent. They are different in that each of the combination are differentially labelled. Examples 7, 8, and 9 provide various examples of the methods of the invention.

The Office states that "...independent claims, as amended, are directed to 'quantitative' methods comprising, *inter alia*, a step of reacting reagents containing aldehyde AND reducing agent. Applicants' specification does not describe methods using labeling reagents containing

aldehyde AND reducing agent, much less 'quantitative' methods using the same."

The Office is encourage to review Examples 7-9 of the instant specification. In these examples, molecules were reacted with various combinations of aldehydes and reducing agents. Also, on page 17 [0090] details are provided for how to accomplish reductive alkylation. As such, there is ample description for one of skill in the art to use an aldehyde and a reducing agent in a quantitative analysis. No undue experimentation would be required. Specific examples of quantitative analysis is taught by Examples 7 to 9 of the specification.

As to the comments in the Office Action regarding lack of teaching for quantitative methods. The claimed methods require that a mass spectrum be obtained on the derivative samples. The use of the mass spectrum in the quantitative analysis is discussed on page 15 [0081] where it is stated:

> The presence of multiplet of peaks of predetermined spacing in the mass spectrum is easily detected and characteristic of peptides from the protein in different samples. The relative intensities of the signals would provide quantitation of the relative amounts of the protein in the different samples.

Thus because the methods require obtaining a mass spectrum, there is adequate teaching of a quantitative analysis.

The Office Action states that there is a "high level of unpredictability in 'quantitative' mass spectrometry" and asserts that there is lack of a reference standard taught.

First, the specification teaches that any number of mass spectrum may be employed. See, for example, page 8 [0033] where a number of mass spectrometry methods are disclosed. The examples go into further detail regarding obtaining the mass spectrum.

Second, Applicants would like to point out that the protein bovine serum albumin (BSA) (see paragraph [0080]) is used as a reference standard and further assert that this is a common protein standard used by those skilled in the art. For example, serum albumin is included in the "Universal Protein Standard" a product of Sigma-Aldrich and is also used as a reference standard

by the Proteomic Standard Research Group of the Association of Biomolecular Resource Facilities. See, http://www.abrf.org/ResearchGroups/ProteomicsStandardsResearchGroup/EPosters/ABRFsPRGStudy2006poster.pdf (copy enclosed herewith).

Third, the present invention creates an internal reference standard through labeling and mixing of multiple samples for each molecule measured. For example, in Figure 13, samples from two forms of fungus were analyzed using the methods of the invention. Depending on the specific purposes of the use, one of the forms of the fungus is chosen as the reference standard and the other sample (or samples) is compared to the reference standard. Figure 10 and the associated description further detail the methods of the invention when 5 samples are compared.

Fourth, the invention avoids the occurrence of differing ionization efficiencies by performing the analysis of multiple samples simultaneously. As found on page 14 [0080], the labelled peptides co-elute during the liquid chromatography separation.

> This is important for accurate quantitation of the samples since peptide intensity in LC-MS analysis is dependent on sample conditions at the time of elution. In other words, relative quantitation requires that peptides co-elute.

Fifth, in contrast to the chemical moieties described in Robbins (U.S. Patent 5,939,229) isotope exchange reactions do not occur with the alkylamine derivatives described for use in the methods of the present invention. The original ratios of the samples (i.e., 3:1:3:1:3) are maintained.

Sixth, and finally, Arend, et al. teaches a method wherein the carbonyl compounds is heated with formaldehyde and an amine hydrochloride in a protic solvent to form a C-C bond. A simplified mechanism is given in Scheme 1 of Arend, et al. The presently claimed invention does not involve heating but it involves the reaction of an amine (not an amine hydrochloride) and further involves formation of a N-C bond.

In light of the above, Applicants assert that the presently claimed invention is adequately described and could be performed without undue experimentation. As such, Applicants respectfully request withdrawal of the rejection.

Claim Rejections under 35 U.S.C. §112 – second paragraph

Claims 4-23 and 32-36 stand rejected under 35 U.S.C. § 112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as their invention.

The Office has rejected the phrase "an aldehyde selected from formaldehyde and acetaldehyde and a reducing agent" as allegedly being indefinite. Applicants have amended the claims to clarify that the combinations of reagents each contain a reducing agent and an aldehyde and that the aldehyde is either formaldehyde or acetaldehyde.

The Office has also rejected a number of other terms in the independent claims. Applicants submit that the amendments submitted herewith, i.e., requiring one combination per sample and that every combination is distinct from each other, obviates this rejection. As such, Applicants request its withdrawal.

Claim Rejections under 35 U.S.C. §102

Initially, to anticipate a claim, a single source must contain all of the elements of the claim. *Hybritech Inc. v. Monoclonal Antibodies, Inc.* 802 F.2d 1367, 1379 (Fed. Cir. 1986). Applicants submit that neither of the references described below teach all of the claimed elements.

1. Aebersold et al.

Claims 4-14, 17-23 and 32-36 stand rejected under 35 U.S.C. §102(e) as allegedly being anticipated by Aebersold et al. (U.S. Patent 6,670,194).

Aebersold et al. teaches a method of analyzing proteins using a multi-component protein reactive reagent of the formula A-L-PRG, where A is an affinity label that selectively binds to a capture reagent, L is a linker group which is differentially labeled with one or more stable isotopes and PRG is a "protein reactive group" that selectively reacts with a protein functional group.

Applicants submit that Aebersold et al. do not provide the requisite teachings of analyzing 3 to 8 samples of molecules by reacting each of the samples with a unique combination of a reducing agent and either formaldehyde or acetaldehyde. While it is generically mentioned in the specification, that more than 2 samples can be analyzed, there is no specific teaching of how this can be accomplished.

Further, Applicants incorporate all previously submitted arguments related to this reference.

Still further, Aebersold et al. refer to the use of "aldehyde and/or ketone reactive groups," however, as correctly pointed out in previous Office Action, there is no specific teaching of formaldehyde nor acetaldehyde. *See,* Aebersold et al., col. 10, lines 37-43. Applicants claims require that one of two the reagents used to label the molecules *must be* an aldehyde selected from formaldehyde or acetaldehyde.

Still further, the Office cites to a deuterated internal standard taught by Aebersold et al. using "B-N(CD_3)CD_2CO-conjugate." *See*, the Office Action at page 11. This is a drastically different molecule than those arrived at by the methods of the invention. First, the "B" in Aebersold refers to Biotin, whereas in the present invention, it would refer to Boron. Biotin is a compound known for affinity capture. Also, the "CD_2CO-" group is a ketone where the present invention uses an aldehyde. Third, the reducing agents taught by the present invention are a cyanoborohydride. There is no cyano group in the internal standard taught by Aebersold et al.

In light of the above, Aebersold et al. do not teach the claimed methods and therefore the reference does not anticipate the claimed invention. Applicants request withdrawal of this rejection.

2. Vandekerckhove & Gevaert

Claims 4-14, 17-23 and 32-36 stand rejected under 35 U.S.C. §102(e) as allegedly being anticipated by Vandekerckhove & Gevaert (U.S. Patent 6,908,740).

Vandekerckhove & Gevaert patent teaches the use of deuterated formaldehyde and acetaldehyde in order to induce a mass distinguishable mass shift in peptide analysis.

Vandekerckhove & Gevaert fails to teach a method of simultaneously quantitatively analyzing 3 to 8 samples of molecules. Despite the use of the phrase "two or more samples" the patent does not describe how this is done. For example, in the same paragraph, the patent describes "...peptides isolated from one sample...peptides isolated from a second sample." There is no mention of a third sample. Similarly, the subsequent paragraphs describe techniques for the analysis of a first sample, a second sample, a first isotope, and a second isotope. There is no description of analyzing 3 to 8 samples using the combination of isotopically unique sets of a reducing agent and formaldehyde or acetaldehyde.

As Vandekerckhove & Gevaert do not teach a method for analyzing 3 to 8 samples using the combinations of agents, this patent does not anticipate the currently claimed invention. Applicants request withdrawal of this rejection.

Conclusion

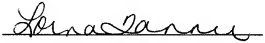
Applicant believes that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested. In the event that this amendment and reply does not place this application in condition for allowance,

Applicants would greatly appreciate if the Examiner would contact the undersigned by telephone at 650-251-1104.

The Commissioner is hereby authorized to charge any additional fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by a check or credit card payment form being in the wrong amount, unsigned, post-dated, otherwise improper or informal or even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741. If any extensions of time are needed for timely acceptance of papers submitted herewith, Applicants hereby petition for such extension under 37 C.F.R. §1.136 and authorizes payment of any such extensions fees to Deposit Account No. 19-0741.

Please direct all correspondence to the undersigned attorney or agent at the address indicated below.

Respectfully submitted,

Date Dec. 18, 2007 By 

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Attorney for Applicants
Registration No. 50,782

CONFORMED CLAIMS
APPENDIX A

Claims 1-3 (canceled)

4. (currently amended) The method of claim 33 comprising an additional step of cleaving the 3 to 8 samples of differential isotope labelled derivatives of molecules into fragments, prior to the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

5. (Currently amended) The method of claim 33 comprising an additional step of denaturing the molecules prior to step (ii).

6. (currently amended) The method of claim 33 wherein the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry comprises introducing the 3 to 8 samples of differential isotope labelled derivatives of molecules to a mass spectrometer using electrospray ionization.

7. (previously presented)The method of claim 6 wherein the electrospray ionization method is selected from the group consisting of nanospray, pneumatically assisted electrospray, ionspray and turboionspray.

8. (currently amended) The method of claim 33 comprising an additional step of separating the 3 to 8 samples of differential isotope labelled derivatives of molecules into sub-fractions before the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

9. (currently amended) The method of claim 8 wherein the step of separating the 3 to 8 samples of differential isotope labelled derivatives of molecules uses a separator selected from the group consisting of 1-D gel electrophoresis, SDS-PAGE, isoelectric focusing, 2-D gel electrophoresis, zone electrophoresis, isotachophoresis, ion exchange chromatography, normal phase chromatography, reverse phase chromatography, hydrophobic interaction chromatography, size exclusion chromatography and any combination of these separators.

10. (currently amended) The method of claim 4 comprising an additional step of separating the fragments after the step of cleaving the 3 to 8 samples of differential isotope labelled derivatives of molecules and before the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules.

11. (previously presented)The method of claim 10 wherein the step of separating the fragments uses a separator selected from the group consisting of liquid chromatography, high performance liquid chromatography and capillary electrophoresis.

12. (currently amended) The method of claim 33 comprising an additional step of analyzing the 3 to 8 samples of differential isotope labelled derivatives of molecules after the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

13. (currently amended) The method of claim 12 wherein the derivatives are peptides and the step of analyzing the 3 to 8 samples of differential isotope labelled derivatives of molecules is selected from the group consisting of collision-induced dissociation in a mass spectrometer operating in MS/MS mode, peptide mass fingerprinting, peptide mapping, Edman sequencing and sequencing by sequential amino acid cleavage.

14. (currently amended) The method of claim 13, comprising an additional step of sequencing the molecules, after the step of analyzing the 3 to 8 samples of differential isotope labelled derivatives of molecules.

15. (canceled)

16. (canceled)

17. (Currently amended) The method of claim 33 wherein the reducing agent is selected from the group consisting of a sodium cyanoborohydride, sodium borohydride, dialkyl borane complexes and pyridine borane complexes.

18. (Currently amended) The method of claim 33 wherein the molecules are selected from the group consisting of cells, cellular extracts, sub-cellular extracts, cellular lysates, peptides, proteins, drugs, toxins, antibodies and pollutants.

19. (previously presented)The method of claim 18 wherein the sample comprises a protein having an amine and the protein is extracted from a cell.

20. (previously presented)The method of claim 19 wherein the amine of the protein is selected from the group consisting of a lysine residue, ornithine residue and a residue at the N- terminal amino group of the protein.

21. (currently amended) The method of claim 33 wherein the step of examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry utilizes a mass spectrometer selected from the group consisting of:

(i) Fourier transform – Ion cyclotron resonance mass spectrometers (FT-ICR-MS);

(ii) Time of Flight mass spectrometers (TOF-MS, TOF-TOF-MS);

(iii) Ion trap mass spectrometers (IT);

(iv) Quadrupole mass spectrometers (Q-MS and QqQ-MS);

(v) Ion mobility mass spectrometers (IM-MS);

(vi) Quadrupole (or hexapole, octapole)-Time of Flight mass spectrometers (Q-TOF, and Qq-TOF); and

(vii) Ion trap – Time of flight mass spectrometers (IT-TOF).

22. (previously presented)The method of claim 21 comprising an additional step of combining the mass spectrometer with an ionization source.

23 (previously presented)The method of claim 22 wherein the ionization source is selected from the group consisting of electrospray ionization, matrix-assisted laser desorption and ionization (MALDI), field desorption, thermal desorption and laser desorption.

Claims 24-32 (canceled)

33. (currently amended) A method for the simultaneous quantitative analysis of 3 to 8 samples comprising molecules, wherein each of the molecules has an amine bearing an active hydrogen, the method comprising:

(i) providing one combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde and acetaldehyde, and each of the combinations of differential isotope reagents is isotopically distinct from each other;

(ii) reacting each of the samples with one of the combination of reagents, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, to provide 3 to 8 samples of differential isotope labelled derivatives of molecules that are differentially isotope labelled from each other at an alkylamine;

(iii) combining the 3 to 8 samples of differential isotope labelled derivatives of the molecules for examination by mass spectrometry; and

(iv) examining the 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

34. (currently amended) A preparation for simultaneous quantitative analysis by mass spectrometry, the preparation comprising 3 to 8 samples of differential isotope labelled derivatives of molecules, said derivatives differentially labelled from each other at an alkylamine resulting from a reduction alkylation of an amine reaction of (a) 3 to 8 samples of molecules having an amine bearing an active hydrogen with (b) a combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde, and each combination of differential isotope labelled reagents is isotopically distinct from each other.

35. (Canceled)

36. (currently amended) A method for the quantitative analysis of 3 to 8 samples of cellular extracts, each of the 3 to 8 samples of cellular extracts comprising molecules having an amine bearing an active hydrogen, the method comprising:

(i) providing one combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde and acetaldehyde, and each of the combinations of differential isotope reagents is isotopically distinct from each other;

(ii) reacting each sample with one of the combinations of differential isotope labelled reagents to produce 3 to 8 samples of differential isotope labelled derivatives of molecules, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, such that the 3 to 8 samples of differential labelled derivatives of molecules are differentially isotope labelled from each other at an alkylamine;

(iii) combining the 3 to 8 samples of differential labelled derivatives of molecules;

(iii) separating the 3 to 8 samples of differential labelled derivatives of molecules into fractions;

(iv) enzymatically cleaving the 3 to 8 samples of differential labelled derivatives of molecules into fragments;

(v) separating the fragments;

(vi) examining the fragments by mass spectrometry; and

(vii) sequencing the fragments.

ABRF-sPRG2006 Study: A Proteomics Standard

P.C. Andrews, D.P. Arnott, M.A. Gawinowicz, J.A. Kowalak, W.S. Lane, K.S. Lilley, L.T. Martin and S.E. Stein
[illegible]

Abstract

[illegible]

The Proteomics Standards Research Group (sPRG) developed the following prototype standard protein mixture, sPRG2006:

[illegible] proteins

5 peptides per protein

Study outcomes:

[illegible] laboratories requested the standard

74 laboratories returned data

[illegible]

Introduction

Why we need a proteomics standard:

- To objectively evaluate a laboratory's ability to perform this type of analysis
- To provide a way for new laboratories to evaluate their performance relative to laboratories with extensive experience
- To be useful for comparative evaluation of instrument performance and bioinformatic analysis of data.

The sPRG2006 standard has been developed to assist in the evaluation of:

- Separation technologies employed in proteomics analysis
- Methodologies used to identify proteins
- Bioinformatics tools used to consolidate protein identifications

Methods

- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]

For more information about this study, please visit

www.abrf.org/sprg

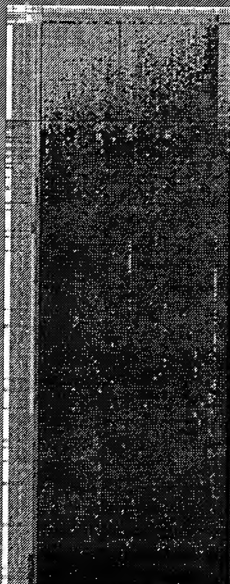


Table 1. Heat Map of Proteins Identified in the sPRG2006 Proteomics Standard

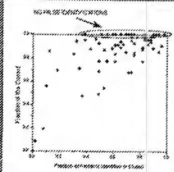
[illegible]

Cells: Number of unique peptides

1 - 2 | 3 - 5 | > 5

Protein Identification Performance for 74 Labs.

[illegible]



Conclusions

- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]
- [illegible]

Acknowledgments

[illegible]

Table 2. Accuracy of Identifications

[illegible]

Protein Identification Summary

[illegible]

Applied Biosystems

Store Log In
Shopping Basket

Home | Products & Services | Support | About Us

Quick Order » Favorites » Workspace » Manage Shopping Baskets »

STORE LOG IN
Username
Password
Log In
New Customer? Register Here
Forgot Your Password?
Forgot Your Username?

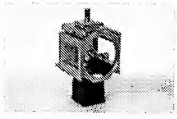
Products & Services

- Cell Biology
- Chromatography
- Custom Primers & Probes
- DNA Sequencing by Capillary Electrophoresis
- DNA Sequencing by Ligation
- DNA Synthesis
- DNA/RNA Modification & Labeling
- DNA/RNA Purification
- Fluorescence Spectrophotometry
- Gene Expression
- Genotyping
- Human Identification & Forensic DNA
- Information Management
- **Mass Spectrometry**
  - Ion Sources
  - Mass Spectrometers
  - Plates & Plate Systems
  - Protein Identification & Quantitation
  - Software
- Microarrays
- MicroRNA Analysis
- Northern/Southern Blotting & Ribonuclease Protection Assays
- PCR/RT-PCR
- Peptide Synthesis
- Protein Sequencing

Products & Services > Mass Spectrometry > Ion Sources > Triple Quadrupole Ion Sources > Ior

IonSpray™ Source

Ordering Information | Product Description | Related Products



The IonSpray source for the API 150*EX*™, API 3000™, and Pulsar systems is an ambient temperature ion source that rates from 1 to 200 µL/min (without flow splitting) and 20(mL/min (with built-in split).

Please Log In to add products to your Shopping Basket/Favorites, **configure a product**, or to available for purchase in your country.

	Product Name	Part Number
☐	IonSpray Arm Assembly for API 150EX™, API 3000™ and QSTAR® Systems	WC015657
☐	IonSpray for API 150EX™, API 3000™ and QSTAR® Systems	WL014615

Note: See user's manual or package insert for limited label license, and trademark information Use Only. Not for use in diagnostics procedures.

Trademark

Quality & Safety Testing
Real-Time PCR
siRNA/RNAi
Services
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